

RECEIVED

JUN 2 4 2002

TECH CENTER 1600/2900

<110> Walke, D. Wade Wilganowski, Nathaniel L. Donoho, Gregory Turner, C. Alexander Jr.

<120> Novel Human Proteases and Polynucleotides Encoding the Same <130> LEX-0114-USA <150> US 60/174,686 <151> 2000-01-06

<170> FastSEQ for Windows Version 4.0

<210> 1 <211> 654 <212> DNA <213> Homo sapien

<400> 1 atgtggacag ctgtgattgg aactaataat atacatggac gctatcctca taccaagaag ъ́0 ataaaaatta aagcaatcat tattcatcca aacttcattt tggaatctta tgtaaatgat 120 180 attgcacttt ttcacttaaa aaaagcagtg aggtataatg actatattca gcctatttgc 240 ctaccttttg atgttttcca aatcctggac ggaaacacaa agtgttttat aagtggctgg 300 ggaagaacaa aagaagaagg taacgctaca aatattttac aagatgcaga agtgcattat atttctcgag agatgtgtaa ttctgagagg agttatgggg gaataattcc taacacttca 360 420 ttttgtgcag gtgatgaaga tggaggtttt gatacttgca ggggtgacag tgggggacca ttaatgtgct acttaccaga atataaaaga ttttttgtaa tgggaattac cagttacgga 480 catggctgtg gtcgaagagg ttttcctggt gtctatattg ggccatcctt ctaccaaaag 540 taggetgacag ageatttett ceatgeaage aeteaaggea taettaetat aaatatttta 600 654 cgtggccaga tecteatage titatgttit gteatettae tageaacaae ataa

<210> 2 <211> 217 <212> PRT <213> Homo sapien

<160> 7

 Met
 Trp
 Thr
 Ala
 Val
 Ile
 Gly
 Thr
 Asn
 Asn
 Ile
 His
 Gly
 Arg
 Tyr
 Pro

 1
 5
 1
 5
 10
 1
 15
 15
 15

 His
 Thr
 Lys
 1le
 Lys
 Ala
 Ile
 Ile
 Ile
 His
 Pro
 Asn
 Phe

 Ile
 Leu
 Glu
 Ser
 Tyr
 Val
 Asn
 Asp
 Ile
 Ala
 Leu
 Phe
 His
 Leu
 Lys
 Lys

 18
 35
 45
 45
 45
 45
 45
 45

4) A Area Christophe (A. C. B. C. B. Y. Man, A. C. Bracanto, C. C. Berg, B. C. Area, A. B. Area (B. C. Bracanto, C. B. C. Bracanto, C. B. C. Bracanto, C. Brac

```
105
                                                    110
            100
Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys Ala Gly Asp Glu Asp Gly
                            120
       115
Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Met Cys Tyr
                        135
Leu Pro Glu Tyr Lys Arg Phe Phe Val Met Gly Ile Thr Ser Tyr Gly
                                       155
                    150
His Gly Cys Gly Arg Arg Gly Phe Pro Gly Val Tyr Ile Gly Pro Ser
                                    170
                165
Phe Tyr Gln Lys Trp Leu Thr Glu His Phe Phe His Ala Ser Thr Gln
                               185
Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly Gln Ile Leu Ile Ala Leu
                            200
Cys Phe Val Ile Leu Leu Ala Thr Thr
    210
                        215
<210> 3
<211> 1047
<212> DNA
<213> Homo sapien
<400> 3
                                                                       61)
atgoggotgg ggotcotgag ogtggogytg ttgtttgtgg ggagototca ottayactca
                                                                       120
gaccactact cgccctctgg aaggcacagg ctcggcccct cgccggaacc ggcggctagt
toccagcagg ctgaggccgt ccgcaagagg ctccggcggc ggagggaggg aggggcgcat
                                                                       130
                                                                       240
qcaaaggatt gtggaacagc accgcttaag gatgtgttgc aagggtctcg gattataggg
                                                                       300
qqqaacqaaq cacaagetgg egcatggeeg tgggtggtga geetgeagat taaatatgge
                                                                       360
equipticity theatgrate teggegeaec chagteagag agageteget ceteacaget
                                                                       400
geocactgea ctaaagaere tagegateet ttaatgtgga cagetgtgat tggaactaat
aatatacatg gacgctatcc tcataccaag aagataaaaa ttaaagcaat cattattcat
                                                                       4 \pm 0
ccaaacttca ttttggaatc ttatgtaaat gatattgcac tttttcactt aaaaaaagca
                                                                       540
                                                                       600
gtqaggtata atgactatat tcagcctatt tgcctacctt ttgatgtttt ccaaatcctg
                                                                       660
gacggaaaca caaagtgttt tataagtggc tggggaagaa caaaagaaga aggtaacgct
                                                                       720
acaaatattt tacaagatgc agaagtgcat tatatttctc gagagatgtg taattctgag
                                                                       730
aggagttatg ggggaataat tootaacact toattitigtg caggigatga agatggaget
tttgatactt gcaggggtga cagtggggga ccattaatgt gctacttacc agaatataaa
                                                                       840
agattttttg taatgggaat taccagttac ggacatggct gtggtcgaag aggttttcct
                                                                       9.50
                                                                       950
ggtgtctata ttgggccatc cttctaccaa aagtggctga cagagcattt cttccatgca
                                                                      1020
agractcaag gratacttae tataaatatt ttacgtggcc agatecteat agetttatgt
                                                                      1047
ittgicator tactagoaac aacataa
<210 > 4
<1111 > 348
<212> PRT
<213> Homo sapien
<400>4
Met Arg Leu Gly Leu Leu Ser Val Ala Leu Leu Phe Val Gly Ser Ser
```

. you was a too a war a war a war a war a word only was a first word by a way of your account of the war and the war a war a war a war and the war a w

70 75 Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val Ser Leu Gln 90 85 Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly Thr Leu Val 100 105 Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys Asp Ala Ser 120 Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn Ile His Gly 130 135 140 Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile Ile Ile His 155 150 1.45 Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala Leu Phe His 165 17 C Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro Ile Cys Leu 185 180 Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys Cys Phe Ile 195 200 Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala Thr Asn Ile Leu 215 220 Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys Asn Ser Glu 230 235 Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys Ala Gly Asp 250 245 Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu 265 260 Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met Gly Ile Thr 280 Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly Val Tyr Ile 295 300 Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe Phe His Ala 315 310 Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly Gln Ile Leu 325 330 Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr 3.45 <210> 5 <211> 867 <212 - DNA -:213 · Homo sapien <1.0 · 5

atgeaaaatt	gtggaadags	accycttaag	gatgtgttgd	aagggtctcg	gattataggg	ΰ.,
ggcaccgaag	cacaagetgg	cgcatggccg	tgggtggtga	gcctgcagat	taaatatggc	120
egtgttettg	ttcatgtatg	tgggggaacc	ctagtgagag	agaggtgggt	cctcacagct	180
geceaetgea	ctaaagacre	tagegatect	ttaatgtgga	cagctgtgat	tggaactaat	240
aatatacatg	gadgetated	tcataccaag	aagataaaaa	ttaaagcaat	cattattcat	300
rcaaacttca	tittggaatc	ttatgtaaat	gatattgcac	tttttcactt	aaaaaaagca	360
ataaaatata	ardactatat	treadedtatt	+4444+4444++	++49+4+++	ddaaatddid	·‡.C

aughthrein den gan de baat en annacht an eilde hat de hieldte dte dat inda alle didt tit ein eile eile eile ei dan dreitung ein de die hat in einternacht alle auch vollt das eila dat hat tille ein ein traf ditale eile eil ad hatteralad einste antha eilt an east at tein eint beneit beneit bedat ein eile eile tit eile eile eile eil <210> 6

<213> Homo sapien

```
<211 > 288
<212> PRT
<213 > Homo sapien
<400> 6
Met Gln Asn Cys Gly Thr Ala Pro Leu Lys Asp Val Leu Gln Gly Ser
               5
                                  10
Arg Ile Ile Gly Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val
                               25
           20
Val Ser Leu Gln Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly
                           40
Gly Thr Leu Val Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr
                       55
                                           60
Lys Asp Ala Ser Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn
                  7.0
                                       75
Asn Ile His Gly Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala
               35
                                   90
Ile Ile Ile His Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile
                              105
           100
Ala Leu Phe His Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln
                           120
       115
Pro Ile Cys Leu Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr
                       135
                                           140
Lys Cys Phe Ile Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala
                                       155
                150
1.45
Thr Asn Ile Leu Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met
                                   170
               165
Cys Asn Ser Glu Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe
           180
                                                   190
                               185
Cys Ala Gly Asp Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser
                           200
                                               205
      195
Gly Gly Pro Leu Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val
                       215
   210
Met Gly Ile Thr Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro
                                       235
                    230
Gly Val Tyr Ile Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His
               245
                                   250
Phe Phe His Ala Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg
                               265
Gly Gln Ile Let Ile Ala Let Cys Phe Val Ile Let Let Ala Thr Thr
                           280
<210 > 7
<211> 1286
<012 - DNA
```

a can a green can tration of a page a activity of a contract and or a gain table and of definite that of a gain a gain of the first of the gain of a gain and a gain of the first of the gain of the g

caccgcttaa	ggatgtgttg	caagggtctc	ggattatagg	gggcaccgaa	gcacaagctg	360
gcgcatggcc	gtgggtggtg	agcctgcaga	ttaaatatgg	ccgtgttctt	gttcatgtat	420
gtgggggaac	cctagtgaga	gagaggtggg	tcctcacagc	tgcccactgc	actaaagacg	480
ctagcgatcc	tttaatgtgg	acagctgtga	ttggaactaa	taatatacat	ggacgctatc	5 4 (
ctcataccaa	gaagataaaa	attaaagcaa	tcattattca	tccaaacttc	attttggaat	500
cttatgtaaa	tgatattgca	ctttttcact	taaaaaaagc	agtgaggtat	aatgactata	ή ή Ú
ttcagcctat	ttgcctacct	tttgatgttt	tccaaatcct	ggacggaaac	acaaagtgtt	720
ttataagtgg	ctggggaaga	acaaaagaag	aaggtaacgc	tacaaatatt	ttacaagatg	780
cagaagtgca	ttatatttct	cgagagatgt	gtaattctga	gaggagttat	gggggaataa	340
ttcctaacac	ttcattttgt	gcaggtgatg	aagatggagc	ttttgatact	tgcaggggtg	900
acagtggggg	accattaatg	tgctacttac	cagaatataa	aagattttt	gtaatgggaa	940
ttaccagtta	cggacatggc	tgtggtcgaa	gaggttttcc	tggtgtctat	attgggccat	1000
ccttctacca	aaagtggctg	acagagcatt	tcttccatgc	aagcactcaa	ggcatactta	1050
ctataaatat	tttacgtggc	cagatcctca	tagctttatg	ttttgtcatc	ttactagcaa	1140
caacataaag	aaattctgaa	ggctttcata	tctttatttt	gcattgtgtc	cctttctatg	1200
ttctatataa	tgaacatcat	ttattcttct	agcaattaat	tgcctacatt	agagatttca	1260
tgtgaacatt	ttatgggcta	taaata				1286